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Using the Topaz Crystallization System to QC Proteins in a Highly Parallel Format. Kyle Self, Andy May, Gang Sun, Shelley Godley, Greg Harris, Kathy Yokobata, Paul Wyatt. Fluidigm Corporation, South San Francisco, CA.

Because Topaz screening chips permit 96 individual crystallization trials with just one microliter of protein, the Topaz system has become the system of choice for proteins that express poorly or are difficult to crystallize.¹ Now, the Topaz system is enabling a new paradigm for crystallization trials wherein crystallizability serves as the primary metric for protein expression and purification.

With the development of the 4.96 chip (four proteins against 96 reagents) and the AutoInspeX[▲] Workstation, the Topaz system has become the standard for a variety of parallel throughput strategies, such as multiple constructs, which accelerate structure determination by giving researchers early access to crystallization data. Data will be presented on the performance of the 4.96 chip, including the detection and classification accuracy from scans taken on Fluidigm's AutoInspeX Workstation, which reduces time spent preparing and analyzing unproductive experiments.

Finally, the recent development of highly parallel chip architectures and relational databases can be used in combination with new screening approaches to further accelerate structure discovery. We will show data collected using a new 8.96 chip and a recently developed Topaz database application that enables researchers to design experiments, identify crystallization conditions, optimize chemistries and translate the results. Combined, these tools enable high throughput crystallization trials which then serve as a standard for selecting proteins for scale-up.

¹ see, e.g., Xiao, Takagi, Collier, Wang, and Springer, *Nature* **432**, 59 (2004).